

1 Paper No. \_\_\_\_\_  
2

3 Filed on behalf of: Senior Party Genetics Institute, LLC  
4

5 By: Kenneth J. Meyers  
6 Leslie A. McDonell  
7 FINNEGAN, HENDERSON, FARABOW,  
8 GARRETT & DUNNER, L.L.P.  
9 901 New York Avenue, NW  
10 Washington, DC 20001-4413  
11 Telephone: 202-408-4000  
12 Facsimile: 202-408-4400  
13 [ken.meyers@finnegan.com](mailto:ken.meyers@finnegan.com)  
14 [leslie.mcdonell@finnegan.com](mailto:leslie.mcdonell@finnegan.com)

15 UNITED STATES PATENT AND TRADEMARK OFFICE

16 BEFORE THE BOARD OF PATENT APPEALS  
17 AND INTERFERENCES

18 Stryker Corporation,  
19 Junior Party,  
20 (Patent 5,266,683,

21 Inventors: Hermann Oppermann, Engin Ozkaynak, Thangavel Kuberanpath,  
22 David C. Rueger, Roy H.L. Pang),  
23

24 v.

25 Genetics Institute, LLC,  
26 Senior Party,  
27 (Application 08/319,831,  
28 Inventors: Rodney M. Hewick, Jack H. Wang,  
29 John M. Wozney, Anthony J. Celeste).  
30

31 Patent Interference 105,508 (RES)  
32 (Technology Center 1600)

33 GENETICS INSTITUTE CLEAN COPY OF CLAIMS  
34

1 Pursuant to the Notice Declaring Interference dated October 6, 2006, Paper No. 1, the  
2 party Genetics Institute, LLC, submits a clean copy of its involved claims pending as of the time  
3 of the declaration of this interference.

4

5

6

Respectfully submitted,

7

8

Dated: October 20, 2006

By: / Kenneth J. Meyers /  
Kenneth J. Meyers  
Registration No. 25,146

9

10

Attorney of Record for Party Genetics  
Institute, LLC

11

12 FINNEGAN, HENDERSON, FARABOW,  
GARRETT & DUNNER, L.L.P.

13 901 New York Avenue, NW  
Washington, DC 20001-4413

14 Telephone: 202-408-4000

15 Facsimile: 202-408-4400

16 ken.meyers@finnegan.com

17

18

19

20

21

22

23

24

1 PATENT INTERFERENCE 105,508 (RES)

2 Genetics Institute, LLC,  
3 Senior Party,  
4 (Application 08/319,831,  
Inventors: Rodney M. Hewick, Jack H. Wang,  
John M. Wozney, Anthony J. Celeste).

5 CLEAN COPY OF CLAIMS

- 6 1. A purified BMP-8 protein characterized by:
- 7 (a) at least one of the following sequences:
- 8 i) Arg-His-Glu-Leu-Tyr-Val-Ser-Phe-Gln-Asp-Leu-Gly-Trp-Leu-Asp-Trp-  
9 Val-Ile-Ala-Pro-Gln-Gly-Tyr (SEQ ID NO: 1);
- 10 ii) Leu-Ser-Ala-Thr-Ser-Val-Leu-Tyr-Tyr-Asp-Ser-Ser-Asn-Asn-Val-Ile-  
11 Leu-Arg (SEQ ID NO: 2); and
- 12 iii) Ala-Cys-Cys-Ala-Pro-Thr-Lys (SEQ ID NO:3);
- 13 (b) a molecular weight of 28,000 - 38,000 daltons as determined by sodium dodecyl  
14 sulfate polyacrylamide gel electrophoresis; and
- 15 (c) a molecular weight of 14,000 - 20,000 daltons under reducing conditions as  
16 determined by sodium dodecyl sulfate polyacrylamide gel electrophoresis said  
protein being a disulfide linked dimer wherein each of the subunits contains the  
sequences set forth in part (a) and said protein having the ability to induce the  
formation of cartilage and/or bone.
- 17 26. A pharmaceutical formulation for bone and/or cartilage formation comprising an  
effective amount of a BMP-8 protein of claim 1 in a pharmaceutically acceptable vehicle.
- 18 27. A composition of claim 26 further comprising a matrix for supporting said composition  
and providing a surface for bone and/or cartilage formation.
- 19 28. The composition of claim 27 wherein said matrix comprises a material selected from the  
group consisting of hydroxyapatite, collagen, polylactic acid and tricalcium phosphate.
- 20 29. A pharmaceutical composition for wound healing and tissue repair said composition  
comprising an effective amount of a BMP-8 protein of claim 1 in a pharmaceutically acceptable  
vehicle.
- 21
- 22
- 23
- 24

**CERTIFICATE OF SERVICE**

I hereby certify that a copy of the foregoing was served on the party Stryker Corporation through its attorney of record on this the 20<sup>th</sup> day of October, 2006 as follows:

**VIA FEDERAL EXPRESS**

6 Kilpatrick & Lockhart Nicholson Graham LLP  
State Street Financial Center  
7 One Lincoln Street  
Boston, MA 02111-2950

Respectfully submitted,

By: / Kenneth J. Meyers /  
Kenneth J. Meyers  
Registration No. 25,146

Attorney of Record for Party Genetics  
Institute, LLC

FINNEGAN, HENDERSON, FARABOW,  
GARRETT & DUNNER, L.L.P.  
901 New York Avenue, NW  
Washington, DC 20001-4413  
Telephone: 202-408-4000  
Facsimile: 202-408-4400  
[ken.meyers@finnegan.com](mailto:ken.meyers@finnegan.com)

Filed on behalf of: Stryker Corporation

Paper No. \_\_\_\_\_

By: James F. Haley, Jr.  
Karen Mangasarian  
Connie Wong  
Fish & Neave IP Group of  
Ropes & Gray LLP  
1251 Avenue of the Americas  
New York, NY 10020  
Tel: 212-596-9000  
Fax: 212-596-9090  
[james.haley@ropesgray.com](mailto:james.haley@ropesgray.com)  
[karen.mangasarian@ropesgray.com](mailto:karen.mangasarian@ropesgray.com)  
[connie.wong@ropesgray.com](mailto:connie.wong@ropesgray.com)

UNITED STATES PATENT AND TRADEMARK OFFICE

---

BEFORE THE BOARD OF PATENT APPEALS  
AND INTERFERENCES

---

**STRYKER CORPORATION,**  
Junior Party  
(Patent 5,266,683,

Inventors: Hermann Oppermann, Engin Ozkaynak, Thangavel Kuberanapath,  
David C. Rueger, Roy H.L. Pang),

v.

**GENETICS INSTITUTE, LLC,**  
Senior Party  
(Application 08/319,831,  
Inventors: Rodney M. Hewick, Jack H. Wang,  
John M. Wozney, Anthony J. Celeste).

---

Patent Interference No. 105,508 (RES)  
(Technology Center 1600)

---

**STRYKER CORPORATION'S CLEAN COPY OF CLAIMS AND SEQUENCES**

STRYKER CORPORATION'S CLEAN COPY OF CLAIMS AND SEQUENCES

1 Pursuant to Bd. R. 110(a), Junior Party Stryker Corporation ("Stryker") submits the  
2 following clean copy of its involved claims of U.S. Patent 5,266,683. Junior Party Stryker also  
3 submits herewith a clean copy of the sequences recited in the involved claims.

Interference No. 105,508 (RES)  
STRYKER CORPORATION v. GENETICS INSTITUTE, LLC

- 1        21. An isolated protein comprising the amino acid sequence described by residues  
2                          306 to 402 of Seq. ID No. 28.
- 3
- 4        22. The protein of claim 21 comprising the amino acid sequence described by  
5                          residues 270-402 of Seq. ID No. 28 (hOP2-Arg).
- 6
- 7        23. The protein of claim 22 comprising the amino acid sequence described by  
8                          residues 267 to 402 of Seq. ID No. 28 (hOP2-Pro).
- 9
- 10      24. The protein of claim 23 comprising the amino acid sequence described by  
11                          residues 264 to 402 of Seq. ID No. 28 (hOP2-Ala).
- 12
- 13      25. The protein of claim 24 comprising the amino acid sequence described by  
14                          residues 243 to 402 of Seq. ID No. 28 (hOP2-Ser).
- 15
- 16      26. The protein of claim 25 comprising the amino acid sequence described by  
17                          residues 1 to 402 of Seq. ID No. 28 (hOP2-PP).
- 18
- 19      27. The protein of claim 6, 15, 18 or 21 capable of inducing cartilage and bone  
20                          formation when implanted in a mammal in association with a matrix.
- 21
- 22      28. Osteogenic protein expressed from recombinant DNA in a host cell,  
23                          the protein comprising a pair of oxidized subunits disulfide bonded to  
24                          produce a dimeric species, one of said subunits having an amino acid sequence  
25                          sufficiently duplicative of the sequence comprising residues 335 to 431 of Seq. ID  
26                          No. 1 (OPS),  
27                          such that the disulfide bonded dimeric species comprising said subunit has  
28                          a conformation capable of inducing cartilage and endochondral bone formation in  
29                          a mammal when disposed within a matrix implanted in said mammal.
- 30
- 31      29. Osteogenic protein expressed from recombinant DNA in a host cell,

1                   the protein comprising a pair of oxidized subunits disulfide bonded to  
2                   produce a dimeric species, having a conformation capable of inducing cartilage  
3                   and endochondral bone formation in a mammal when disposed within a matrix  
4                   implanted in said mammal,

5                   one of said subunits having an amino acid sequence encoded by a nucleic  
6                   acid capable of hybridizing to a nucleic acid encoding OPS (res. 335-431, Seq. ID  
7                   No. 1) under stringent hybridization conditions.

8

9                 39. The protein of claim 28 or 29 wherein said subunit comprises at least the  
10                  osteogenically active region of a protein selected from the group consisting of:  
11                  mOP1-PP (residues 1-430, Seq. ID No. 24); mOP2-PP (residues 1-399 of Seq. ID  
12                  No. 26); and hOP2-PP (residues 1-402 of Seq. ID No. 28).

13

14                 45. An isolated polypeptide chain useful as a subunit of a dimeric osteogenic protein,  
15                  said polypeptide chain having an amino acid sequence sharing greater than 74%  
16                  identity with the sequence described by residues 264-402 of Seq. ID No. 28  
17                  (hOP2-Ala) such that the disulfide bonded dimeric species comprising said  
18                  polypeptide chain is capable of inducing endochondral bone formation when  
19                  implanted in a mammal in association with a matrix.

20

21                 46. An isolated polypeptide chain useful as a subunit of a dimeric osteogenic protein  
22                  having a conformation capable of inducing endochondral bone formation in a  
23                  mammal when implanted in a mammal in association with a matrix,

24                   said polypeptide chain having an amino acid sequence encoded by a  
25                  nucleic acid capable of hybridizing to a nucleic acid encoding the pro region of  
26                  mOP2-PP (res. 17-260 of Seq. ID No. 26) or hOP2-PP (res. 17-263 of Seq. ID  
27                  No. 28) under stringent hybridization conditions.

28

29                 47. The polypeptide chain of claim 45 or 46 having an amino acid sequence sharing  
30                  greater than 80% identity with the amino acid sequence of hOP2-Ala.

48. The polypeptide chain of claim 47 having an amino acid sequence sharing greater than 85% identity with the amino acid sequence of hOP2-Ala.

49. The polypeptide chain of claim 45 or 46 wherein said amino acid sequence is selected from the group consisting of: mOP2-Ala (residues 261-399 Seq. ID No. 26); hOP2-Ala (residues 264-402 of Seq. ID No. 28); hOP2-Pro (residues 267-402 of Seq. ID No. 28); hOP2-Arg (residues 270-402 of Seq. ID No. 28) and hOP2-Ser (residues 243-402 of Seq. ID No. 28).

50. The polypeptide chain of claim 45 or 46 wherein said amino acid sequence is derived from an amino acid sequence selected from the group consisting of: mOP2-PP (residues 1-399 of Seq. ID No. 26) and hOP2-PP (residues 1-402 of Seq. ID No. 28) including allelic variants thereof, and natural and biosynthetic mutants thereof.

51. The polypeptide chain of claim 45 or 46 that is glycosylated.

52. An isolated dimeric protein capable of inducing cartilage or endochondral bone formation in a mammal when implanted in said mammal in association with a matrix,  
said protein comprising a pair of disulfide-bonded polypeptide chains constituting a dimeric species, wherein each said polypeptide chain is the polypeptide chain of claim 45 or 46.

53. The dimeric protein of claim 52 wherein each said polypeptide chain is independently selected and comprises at least the osteogenically active region of mOP2-PP (residues 1-399 of Seq. ID No. 26) or hOP2-PP (residues 1-402 of Seq. ID No. 28).

54. The dimeric protein of claim 53, wherein each said polypeptide chain is independently selected from the group consisting of: mOP2-Ala (residues 261-399 Seq. ID No. 26); hOP2-Ala (residues 264-402 of Seq. ID No. 28); hOP2-Pro

1                   (residues 267-402 of Seq. ID No. 28); hOP2-Arg (residues 270-402 of Seq. ID  
2                   No. 28) and hOP2-Ser (residues 243-402 of Seq. ID No. 28).

3

4       58. A protein expressed from recombinant DNA in a host cell, said protein  
5                   comprising an amino acid sequence encoded by a nucleic acid capable of  
6                   hybridizing to a nucleic acid encoding residues 306-402 of hOP2 (Seq. ID No. 28)  
7                   under stringent hybridization conditions.

8

9

Interference No. 105,508 (RES)  
STRYKER CORPORATION v. GENETICS INSTITUTE, LLC

1  
2  
3 SEQUENCE DESCRIPTION: SEQ ID NO:1:  
4  
5 GGTGCGGGCC CGGAGCCCGG AGCCCGGGTA GCGCGTAGAG CCGGCGCG ATG CAC GTG 57  
6 Met His Val  
7 1  
8  
9 CGC TCA CTG CGA GCT GCG GCG CCG CAC AGC TTC GTG GCG CTC TGG GCA 105  
10 Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala Leu Trp Ala  
11 5 10 15  
12  
13 CCC CTG TTC CTG CTG CGC TCC GCC CTG GCC GAC TTC AGC CTG GAC AAC 153  
14 Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser Leu Asp Asn  
15 20 25 30 35  
16  
17 GAG GTG CAC TCG AGC TTC ATC CAC CGG CGC CTC CGC AGC CAG GAG CGG 201  
18 Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser Gln Glu Arg  
19 40 45 50  
20  
21 CGG GAG ATG CAG CGC GAG ATC CTC TCC ATT TTG GGC TTG CCC CAC CGC 249  
22 Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu Pro His Arg  
23 55 60 65  
24  
25 CCG CGC CCG CAC CTC CAG GGC AAG CAC AAC TCG GCA CCC ATG TTC ATG 297  
26 Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro Met Phe Met  
27 70 75 80  
28  
29 CTG GAC CTG TAC AAC GCC ATG GCG GTG GAG GAG GGC GGC GGG CCC GGC 345  
30 Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly Pro Gly  
31 85 90 95  
32  
33 GGC CAG GGC TTC TCC TAC CCC TAC AAG GCC GTC TTC AGT ACC CAG GGC 393  
34 Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser Thr Gln Gly  
35 100 105 110 115  
36  
37 CCC CCT CTG GCC AGC CTG CAA GAT AGC CAT TTC CTC ACC GAC GCC GAC 441  
38 Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr Asp Ala Asp  
39 120 125 130  
40  
41 ATG GTC ATG AGC TTC GTC AAC CTC GTG GAA CAT GAC AAG GAA TTC TTC 489  
42 Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys Glu Phe Phe  
43 135 140 145  
44  
45 CAC CCA CGC TAC CAC CAT CGA GAG TTC CGG TTT GAT CTT TCC AAG ATC 537  
46 His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu Ser Lys Ile  
47 150 155 160  
48  
49 CCA GAA GGG GAA GCT GTC ACG GCA GCC GAA TTC CGG ATC TAC AAG GAC 585  
50 Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Asp  
51 165 170 175  
52  
53 TAC ATC CGG GAA CGC TTC GAC AAT GAG ACG TTC CGG ATC AGC GTT TAT 633  
54 Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile Ser Val Tyr  
55 180 185 190 195  
56  
57 CAG GTG CTC CAG GAG CAC TTG GGC AGG GAA TCG GAT CTC TTC CTG CTC 681

1	Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu Phe Leu Leu		
2	200	205	210
3			
4	GAC AGC CGT ACC CTC TGG GCC TCG GAG GAG GGC TGG CTG GTG TTT GAC	729	
5	Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu Val Phe Asp		
6	215	220	225
7			
8	ATC ACA GCC ACC AGC AAC CAC TGG GTG GTC AAT CCG CGG CAC AAC CTG	777	
9	Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg His Asn Leu		
10	230	235	240
11			
12	GGC CTG CAG CTC TCG GTG GAG ACG CTG GAT GGG CAG AGC ATC AAC CCC	825	
13	Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser Ile Asn Pro		
14	245	250	255
15			
16	AAG TTG GCG GGC CTG ATT GGG CGG CAC GGG CCC CAG AAC AAG CAG CCC	873	
17	Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn Lys Gln Pro		
18	260	265	270
19			275
20	TTC ATG GTG GCT TTC TTC AAG GCC ACG GAG GTC CAC TTC CGC AGC ATC	921	
21	Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe Arg Ser Ile		
22	280	285	290
23			
24	CGG TCC ACG GGG AGC AAA CAG CGC AGC CAG AAC CGC TCC AAG ACG CCC	969	
25	Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser Lys Thr Pro		
26	295	300	305
27			
28	AAG AAC CAG GAA GCC CTG CGG ATG GCC AAC GTG GCA GAG AAC AGC AGC	1017	
29	Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu Asn Ser Ser		
30	310	315	320
31			
32	AGC GAC CAG AGG CAG GCC TGT AAG AAG CAC GAG CTG TAT GTC AGC TTC	1065	
33	Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe		
34	325	330	335
35			
36	CGA GAC CTG GGC TGG CAG GAC TGG ATC ATC GCG CCT GAA GGC TAC GCC	1113	
37	Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala		
38	340	345	350
39			355
40	GCC TAC TAC TGT GAG GGG GAG TGT GCC TTC CCT CTG AAC TCC TAC ATG	1161	
41	Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met		
42	360	365	370
43			
44	AAC GCC ACC AAC CAC GCC ATC GTG CAG ACG CTG GTC CAC TTC ATC AAC	1209	
45	Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn		
46	375	380	385
47			
48	CCG GAA ACG GTG CCC AAG CCC TGC TGT GCG CCC ACG CAG CTC AAT GCC	1257	
49	Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala		
50	390	395	400
51			
52	ATC TCC GTC CTC TAC TTC GAT GAC AGC TCC AAC GTC ATC CTG AAG AAA	1305	
53	Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys		
54	405	410	415
55			
56	TAC AGA AAC ATG GTG GTC CGG GCC TGT GGC TGC CAC TAGCTCCTCC	1351	
57	Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His		
58	420	425	430

Interference No. 105,508 (RES)  
STRYKER CORPORATION v. GENETICS INSTITUTE, LLC

1 GAGAATTCA G ACCCTTG GGG GCCAAGTTT TCTGGATCCT CCATTGCTCG CCTTGGCCAG 1411  
2 GAACCAGCAG ACCAACTGCC TTTGTGAGA CCTTCCCCTC CCTATCCCCA ACTTTAAAGG  
3 4  
5 6 TGTGAGAGTA TTAGGAAACA TGAGCAGCAT ATGGCTTTG ATCAGTTTT CAGTGGCAGC 1531  
7 8 ATCCAATGAA CAAGATCCTA CAAGCTGTGC AGGCAAAACC TAGCAGGAAA AAAAAACAAAC 1591  
9 10 GCATAAAGAA AAATGGCCGG GCCAGGTCA TGGCTGGAA GTCTCAGCCA TGCACGGACT 1651  
11 12 CGTTTCCAGA GGTAATTATG AGCGCCTACC AGCCAGGCCA CCCAGCCGTG GGAGGAAGGG 1711  
13 14 GGC GTGGCAA GGGGTGGCA CATTGGTGTG TGTGCGAAAG GAAAATTGAC CCGGAAGTTC 1771  
15 16 CTGTAATAAA TGTCACAATA AACGAATGA ATGAAAAAAA AAAAAAAA A 1822  
17 18  
19 20  
21 SEQUENCE DESCRIPTION: SEQ ID NO:24:  
22  
23 CTGCAGCAAG TGACCTCGGG TCGTGGACCG CTGCCCTGCC CCCTCCGCTG CCACCTGGGG 60  
24  
25 CGGCGCGGGC CCGGTGCCCG GGATCGCGCG TAGAGCCGGC GCG ATG CAC GTG CGC 115  
26 Met His Val Arg  
27 1  
28  
29 TCG CTG CGC GCT GCG GCG CCA CAC AGC TTC GTG GCG CTC TGG GCG CCT 163  
30 Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala Leu Trp Ala Pro  
31 5 10 15 20  
32  
33 CTG TTC TTG CTG CGC TCC GCC CTG GCC GAT TTC AGC CTG GAC AAC GAG 211  
34 Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser Leu Asp Asn Glu  
35 25 30 35  
36  
37 GTG CAC TCC AGC TTC ATC CAC CGG CGC CTC CGC AGC CAG GAG CGG CGG 259  
38 Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser Gln Glu Arg Arg  
39 40 45 50  
40  
41 GAG ATG CAG CGG GAG ATC CTG TCC ATC TTA GGG TTG CCC CAT CGC CCG 307  
42 Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu Pro His Arg Pro  
43 55 60 65  
44  
45 CGC CCG CAC CTC CAG GGA AAG CAT AAT TCG GCG CCC ATG TTC ATG TTG 355  
46 Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro Met Phe Met Leu  
47 70 75 80  
48  
49 GAC CTG TAC AAC GCC ATG GCG GTG GAG GAG AGC GGG CCG GAC GGA CAG 403  
50 Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Ser Gly Pro Asp Gly Gln  
51 85 90 95 100  
52  
53 GGC TTC TCC TAC CCC TAC AAG GCC GTC TTC AGT ACC CAG GGC CCC CCT 451  
54 Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser Thr Gln Gly Pro Pro  
55 105 110 115  
56  
57 TTA GCC AGC CTG CAG GAC AGC CAT TTC CTC ACT GAC GCC GAC ATG GTC 499  
58 Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr Asp Ala Asp Met Val

Interference No. 105,508 (RES)  
 STRYKER CORPORATION v. GENETICS INSTITUTE, LLC

1	120	125	130	
2				
3	ATG AGC TTC GTC AAC CTA GTG GAA CAT GAC AAA GAA TTC TTC CAC CCT			547
4	Met Ser Phe Val Asn Leu Val Glu His Asp Lys Glu Phe Phe His Pro			
5	135	140	145	
6				
7	CGA TAC CAC CAT CGG GAG TTC CGG TTT GAT CTT TCC AAG ATC CCC GAG			595
8	Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu Ser Lys Ile Pro Glu			
9	150	155	160	
10				
11	GGC GAA CGG GTG ACC GCA GCC GAA TTC AGG ATC TAT AAG GAC TAC ATC			643
12	Gly Glu Arg Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Asp Tyr Ile			
13	165	170	175	180
14				
15	CGG GAG CGA TTT GAC AAC GAG ACC TTC CAG ATC ACA GTC TAT CAG GTG			691
16	Arg Glu Arg Phe Asp Asn Glu Thr Phe Gln Ile Thr Val Tyr Gln Val			
17	185	190	195	
18				
19	CTC CAG GAG CAC TCA GGC AGG GAG TCG GAC CTC TTC TTG CTG GAC AGC			739
20	Leu Gln Glu His Ser Gly Arg Glu Ser Asp Leu Phe Leu Leu Asp Ser			
21	200	205	210	
22				
23	CGC ACC ATC TGG GCT TCT GAG GAG GGC TGG TTG GTG TTT GAT ATC ACA			787
24	Arg Thr Ile Trp Ala Ser Glu Glu Gly Trp Leu Val Phe Asp Ile Thr			
25	215	220	225	
26				
27	GCC ACC AGC AAC CAC TGG GTG GTC AAC CCT CCG CAC AAC CTG GGC TTA			835
28	Ala Thr Ser Asn His Trp Val Val Asn Pro Arg His Asn Leu Gly Leu			
29	230	235	240	
30				
31	CAG CTC TCT GTG GAG ACC CTG GAT GGG CAG AGC ATC AAC CCC AAG TTG			883
32	Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser Ile Asn Pro Lys Leu			
33	245	250	255	260
34				
35	GCA GGC CTG ATT GGA CGG CAT GGA CCC CAG AAC AAG CAA CCC TTC ATG			931
36	Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn Lys Gln Pro Phe Met			
37	265	270	275	
38				
39	GTG GCC TTC TTC AAG GCC ACG GAA GTC CAT CTC CGT AGT ATC CGG TCC			979
40	Val Ala Phe Phe Lys Ala Thr Glu Val His Leu Arg Ser Ile Arg Ser			
41	280	285	290	
42				
43	ACG GGG GGC AAG CAG CGC AGC CAG AAT CGC TCC AAG ACG CCA AAG AAC			1027
44	Thr Gly Gly Lys Gln Arg Ser Gln Asn Arg Ser Lys Thr Pro Lys Asn			
45	295	300	305	
46				
47	CAA GAG GCC CTG AGG ATG GCC AGT GTG GCA GAA AAC AGC AGC AGT GAC			1075
48	Gln Glu Ala Leu Arg Met Ala Ser Val Ala Glu Asn Ser Ser Ser Asp			
49	310	315	320	
50				
51	CAG AGG CAG GCC TGC AAG AAA CAT GAG CTG TAC GTC AGC TTC CGA GAC			1123
52	Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg Asp			
53	325	330	335	340
54				
55	CTT GGC TGG CAG GAC TGG ATC ATT GCA CCT GAA GGC TAT GCT GCC TAC			1171
56	Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala Tyr			
57	345	350	355	
58				

1	TAC TGT GAG GGA GAG TGC GCC TTC CCT CTG AAC TCC TAC ATG AAC GCC	1219
2	Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met Asn Ala	
3	360 365 370	
4		
5	ACC AAC CAC GCC ATC GTC CAG ACA CTG GTT CAC TTC ATC AAC CCA GAC	1267
6	Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn Pro Asp	
7	375 380 385	
8		
9	ACA GTA CCC AAG CCC TGC TGT GCG CCC ACC CAG CTC AAC GCC ATC TCT	1315
10	Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala Ile Ser	
11	390 395 400	
12		
13	GTC CTC TAC TTC GAC GAC AGC TCT AAT GTC ATC CTG AAG AAG TAC AGA	1363
14	Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr Arg	
15	405 410 415 420	
16		
17	AAC ATG GTG GTC CGG GCC TGT GGC TGC CAC TAGCTCTGCC TGAGACCCTG	1413
18	Asn Met Val Val Arg Ala Cys Gly Cys His	
19	425 430	
20		
21	ACCTTTGCGGG GGCCACACCT TTCCAAATCT TCGATGTCTC ACCATCTAAG TCTCTCACTG	1473
22		
23	CCCACCTTGG CGAGGAGAAC AGACCAACCT CTCCTGAGCC TTCCCTCACCC TCCCAACCGG	1533
24		
25	AAGCATGTAA GGGTTCCAGA AACCTGAGCG TGCAGCAGCT GATGAGCGCC CTTTCCTTCT	1593
26		
27	GGCACGTGAC GGACAAGATC CTACCAGCTA CCACAGCAAA CGCCTAAGAG CAGGAAAAAT	1653
28		
29	GTCTGCCAGG AAAGTGTCCA GTGTCCACAT GGCCCCTGGC GCTCTGAGTC TTTGAGGAGT	1713
30		
31	AATCGCAAGC CTCGTTCAAGC TGCAGCAGAA GGAAGGGCTT AGCCAGGGTG GGCGCTGGCG	1773
32		
33	TCTGTGTTGA AGGGAAACCA AGCAGAAGCC ACTGTAATGA TATGTCACAA TAAAACCCAT	1833
34		
35	GAATGAAAAA AAAAAAAAAA AAAAAAAAAA AAAAGAATTG	1873
36		
37		
38		
39		
40	<b>SEQUENCE DESCRIPTION: SEQ ID NO:26:</b>	
41		
42	gaattccgct gccaggcaca ggtgcgcgcgt ctggcctcc ccgtctggcg tcagccgagc	60
43		
44	ccgaccagct accagtggat gcgcgcggc tgaaagtccg ag atg gct atg cgt	114
45	Met Ala Met Arg	
46	1	
47		
48	ccc ggg cca ctc tgg cta ttg ggc ctt gct ctg tgc gcg ctg gga ggc	162
49	Pro Gly Pro Leu Trp Leu Leu Gly Leu Ala Leu Cys Ala Leu Gly Gly	
50	5 10 15 20	
51		
52	ggc cac ggt ccc ggt ccc ccg cac acc tgt ccc cag cgt cgc ctg gga	210
53	Gly His Gly Pro Gly Pro Pro His Thr Cys Pro Gln Arg Arg Leu Gly	
54	25 30 35	
55		
56	gct cgc gac cgg gac atg cag cgt gaa atc ctg ccg gtg ctc ggg cta	258
57	Ala Arg Asp Arg Asp Met Gln Arg Glu Ile Leu Pro Val Leu Gly Leu	
58	40 45 50	

Interference No. 105,508 (RES)  
**STRYKER CORPORATION v. GENETICS INSTITUTE, LLC**

1 ccg gga cgc ccc gac ccc gtg cac aac ccg ccg ctg ccc ggc acg cag 306  
 2 Pro Gly Arg Pro Asp Pro Val His Asn Pro Pro Leu Pro Gly Thr Gln  
 3 55 60 65  
 4  
 5  
 6 cgt gcg ccc ctc ttc atg ttg gac cta tac cac gcc atg acc gat gac 354  
 7 Arg Ala Pro Leu Phe Met Leu Asp Leu Tyr His Ala Met Thr Asp Asp  
 8 70 75 80  
 9  
 10 gac gac ggc ggg cca cca cag gct cac tta ggc cgt gcc gac ctg gtc 402  
 11 Asp Asp Gly Gly Pro Pro Gln Ala His Leu Gly Arg Ala Asp Leu Val  
 12 85 90 95 100  
 13  
 14 atg agc ttc gtc aac atg gtg gaa cgc gac cgt acc ctg ggc tac cag 450  
 15 Met Ser Phe Val Asn Met Val Glu Arg Asp Arg Thr Leu Gly Tyr Gln  
 16 105 110 115  
 17  
 18 gag cca cac tgg aag gaa ttc cac ttt gac cta acc cag atc cct gct 498  
 19 Glu Pro His Trp Lys Glu Phe His Phe Asp Leu Thr Gln Ile Pro Ala  
 20 120 125 130  
 21  
 22 ggg gag gct gtc aca gct gct gag ttc cgg atc tac aaa gaa ccc agc 546  
 23 Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Glu Pro Ser  
 24 135 140 145  
 25  
 26 acc cac ccg ctc aac aca acc ctc cac atc agc atg ttc gaa gtg gtc 594  
 27 Thr His Pro Leu Asn Thr Leu His Ile Ser Met Phe Glu Val Val  
 28 150 155 160  
 29  
 30 caa gag cac tcc aac agg gag tct gac ttg ttc ttt ttg gat ctt cag 642  
 31 Gln Glu His Ser Asn Arg Glu Ser Asp Leu Phe Leu Asp Leu Gln  
 32 165 170 175 180  
 33  
 34 acg ctc cga tct ggg gac gag ggc tgg ctg gtg ctg gac atc aca gca 690  
 35 Thr Leu Arg Ser Gly Asp Glu Gly Trp Leu Val Leu Asp Ile Thr Ala  
 36 185 190 195  
 37  
 38 gcc agt gac cga tgg ctg ctg aac cat cac aag gac ctg gga ctc cgc 738  
 39 Ala Ser Asp Arg Trp Leu Leu Asn His His Lys Asp Leu Gly Leu Arg  
 40 200 205 210  
 41  
 42 ctc tat gtg gaa acc gcg gat ggg cac agc atg gat cct ggc ctg gct 786  
 43 Leu Tyr Val Glu Thr Ala Asp Gly His Ser Met Asp Pro Gly Leu Ala  
 44 215 220 225  
 45  
 46 ggt ctg ctt gga cga caa gca cca cgc tcc aga cag cct ttc atg gta 834  
 47 Gly Leu Leu Gly Arg Gln Ala Pro Arg Ser Arg Gln Pro Phe Met Val  
 48 230 235 240  
 49  
 50 acc ttc ttc agg gcc agc cag agt cct gtg cgg gcc cct cgg gca gcg 882  
 51 Thr Phe Phe Arg Ala Ser Gln Ser Pro Val Arg Ala Pro Arg Ala Ala  
 52 245 250 255 260  
 53  
 54 aga cca ctg aag agg agg cag cca aag aaa acg aac gag ctt ccg cac 930  
 55 Arg Pro Leu Lys Arg Arg Gln Pro Lys Lys Thr Asn Glu Leu Pro His  
 56 265 270 275  
 57  
 58 ccc aac aaa ctc cca ggg atc ttt gat gat ggc cac ggt tcc cgc ggc 978

1	Pro Asn Lys Leu Pro Gly Ile Phe Asp Asp Gly His Gly Ser Arg Gly		
2	280	285	290
3			
4	aga gag gtt tgc cgc agg cat gag ctc tac gtc aga ttc cgt gac ctt		1026
5	Arg Glu Val Cys Arg Arg His Glu Leu Tyr Val Arg Phe Arg Asp Leu		
6	295	300	305
7			
8	ggc tgg ctg gac tgg gtc atc gcc ccc cag ggc tac tct gcc tat tac		1074
9	Gly Trp Leu Asp Trp Val Ile Ala Pro Gln Gly Tyr Ser Ala Tyr Tyr		
10	310	315	320
11			
12	tgt gag ggg gag tgt gct ttc cca ctg gac tcc tgt atg aac gcc acc		1122
13	Cys Glu Gly Glu Cys Ala Phe Pro Leu Asp Ser Cys Met Asn Ala Thr		
14	325	330	335
15			
16	aac cat gcc atc ttg cag tct ctg gtg cac ctg atg aag cca gat gtt		1170
17	Asn His Ala Ile Leu Gln Ser Leu Val His Leu Met Lys Pro Asp Val		
18	345	350	355
19			
20	gtc ccc aag gca tgc tgt gca ccc acc aaa ctg agt gcc acc tct gtg		1218
21	Val Pro Lys Ala Cys Cys Ala Pro Thr Lys Leu Ser Ala Thr Ser Val		
22	360	365	370
23			
24	ctg tac tat gac agc agc aac aat gtc atc ctg cgt aaa cac cgt aac		1266
25	Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile Leu Arg Lys His Arg Asn		
26	375	380	385
27			
28	atg gtg gtc aag gcc tgt ggc tgc cac tgaggccccg cccagcatcc		1313
29	Met Val Val Lys Ala Cys Gly Cys His		
30	390	395	
31			
32	tgcttctact accttaccat ctggccgggc ccctctccag aggcagaaac ccttcttatgt		1373
33			
34	tatcatagct cagacagggg caatggagg cccttcactt cccctggcca cttcctgcta		1433
35			
36	aaattctgggt ctttcccagt tcctctgtcc ttcatgggtt ttcggggcta tcaccccgcc		1493
37			
38	ctctccatcc tcctacccca agcatagact gaatgcacac agcatccag agctatgcta		1553
39			
40	actgagaggt ctggggtcag cactgaaggc ccacatgagg aagactgatc cttggccatc		1613
41			
42	ctcagcccac aatggcaaat tctggatggt ctaagaagcc ctggattct aaactagatg		1673
43			
44	atctgggctc tctgcaccat tcattgtggc agttggaca ttttaggta taacagacac		1733
45			
46	atacacttag atcaatgcat cgctgtactc cttgaaatca gagctagctt gttaaaaaaa		1793
47			
48	gaatcagagc caggtatagc ggtgcattgc attaatccca gcgctaaaga gacagagaca		1853
49			
50	ggagaatctc tgtgagttca aggccacata gaaagagcct gtctcgggag cagaaaaaaa		1913
51			
52	aaaaaaaaacg gaattc		1929
53			
54			
55			
56			
57	SEQUENCE DESCRIPTION: SEQ ID NO:28:		
58			

1	GGCGCCGGCA GAGCAGGAGT GGCTGGAGGA GCTGTGGTTG GAGCAGGAGG TGGCACGGCA	60
2	GGGCTGGAGG GCTCCCTATG AGTGGCGGAG ACGGCCAGG AGGCGCTGGA GCAACAGCTC	120
3	CCACACCGCA CCAAGCGGTG GCTGCAGGAG CTCGCCATC GCCCTGCAG TGCTCGGACC	180
4	GCGGCCACAG CGGGACTGGC GGGTACGGCG GCGACAGAGG CATTGGCCGA GAGTCCCAGT	240
5	CCGCAGAGTA GCCCCGGCCT CGAGGCGGTG GCGTCCCGGT CCTCTCCGTC CAGGAGCCAG	300
6	GACAGGTGTC GCGCGGCCGG GCTCCAGGGA CCGCGCCTGA GGCCGGCTGC CCGCCCGTCC	360
7	CGCCCCGCC CGCCGCCCGC CGCCCGCCGA GCCCAGCCTC CTTGCCGTG GGGCGTCCCC	420
8	AGGCCCTGGG TCGGCCGCGG AGCCGATGCG CGCCCGCTGA GCGCCCCAGC TGAGCGCCCC	480
9	CGGCCTGCC ATG ACC GCG CTC CCC GGC CCG CTC TGG CTC CTG GGC CTG	528
10	Met Thr Ala Leu Pro Gly Pro Leu Trp Leu Leu Gly Leu	
11	1 5 10	
12	GCG CTA TGC GCG CTG GGC GGG GGC GGC CCC GGC CTG CGA CCC CCG CCC	576
13	Ala Leu Cys Ala Leu Gly Gly Gly Pro Gly Leu Arg Pro Pro Pro	
14	15 20 25	
15	GGC TGT CCC CAG CGA CGT CTG GGC GCG CGC GAG CGC CGG GAC GTG CAG	624
16	Gly Cys Pro Gln Arg Arg Leu Gly Ala Arg Glu Arg Arg Asp Val Gln	
17	30 35 40 45	
18	CGC GAG ATC CTG GCG GTG CTC GGG CTG CCT GGG CGG CCC CGG CCC CGC	672
19	Arg Glu Ile Leu Ala Val Leu Gly Leu Pro Gly Arg Pro Arg Pro Arg	
20	31 50 55 60	
21	GCG CCA CCC GCC TCC CGG CTG CCC GCG TCC GCG CCG CTC TTC ATG	720
22	Ala Pro Pro Ala Ala Ser Arg Leu Pro Ala Ser Ala Pro Leu Phe Met	
23	35 65 70 75	
24	CTG GAC CTG TAC CAC GCC ATG GCC GGC GAC GAC GAG GAC GGC GCG	768
25	Leu Asp Leu Tyr His Ala Met Ala Gly Asp Asp Asp Glu Asp Gly Ala	
26	39 80 85 90	
27	CCC GCG GAG CGG CGC CTG GGC CGC GCC GAC CTG GTC ATG AGC TTC GTT	816
28	Pro Ala Glu Arg Arg Leu Gly Arg Ala Asp Leu Val Met Ser Phe Val	
29	43 95 100 105	
30	AAC ATG GTG GAG CGA GAC CGT GCC CTG GGC CAC CAG GAG CCC CAT TGG	864
31	Asn Met Val Glu Arg Asp Arg Ala Leu Gly His Gln Glu Pro His Trp	
32	47 110 115 120 125	
33	AAG GAG TTC CGC TTT GAC CTG ACC CAG ATC CCG GCT GGG GAG GCG GTC	912
34	Lys Glu Phe Arg Phe Asp Leu Thr Gln Ile Pro Ala Gly Glu Ala Val	
35	51 130 135 140	
36	ACA GCT GCG GAG TTC CGG ATT TAC AAG GTG CCC AGC ATC CAC CTG CTC	960
37	Thr Ala Ala Glu Phe Arg Ile Tyr Lys Val Pro Ser Ile His Leu Leu	
38	54 145 150 155	
39	AAC AGG ACC CTC CAC GTC AGC ATG TTC CAG GTG GTC CAG GAG CAG TCC	1008
40	Asn Arg Thr Leu His Val Ser Met Phe Gln Val Val Gln Glu Gln Ser	

Interference No. 105,508 (RES)  
 STRYKER CORPORATION v. GENETICS INSTITUTE, LLC

1	160	165	170	
2				
3	AAC AGG GAG TCT GAC TTG TTC TTT TTG GAT CTT CAG ACG CTC CGA GCT Asn Arg Glu Ser Asp Leu Phe Phe Leu Asp Leu Gln Thr Leu Arg Ala			1056
4	175	180	185	
5				
6				
7	GGA GAC GAG GGC TGG CTG GTG CTG GAT GTC ACA GCA GCC AGT GAC TGC Gly Asp Glu Gly Trp Leu Val Leu Asp Val Thr Ala Ala Ser Asp Cys			1104
8	190	195	200	205
9				
10				
11	TGG TTG CTG AAG CGT CAC AAG GAC CTG GGA CTC CGC CTC TAT GTG GAG Trp Leu Leu Lys Arg His Lys Asp Leu Gly Leu Arg Leu Tyr Val Glu			1152
12	210	215	220	
13				
14				
15	ACT GAG GAC GGG CAC AGC GTG GAT CCT GGC CTG GCC GGC CTG CTG GGT Thr Glu Asp Gly His Ser Val Asp Pro Gly Leu Ala Gly Leu Leu Gly			1200
16	225	230	235	
17				
18				
19	CAA CGG GCC CCA CGC TCC CAA CAG CCT TTC GTG GTC ACT TTC TTC AGG Gln Arg Ala Pro Arg Ser Gln Gln Pro Phe Val Val Thr Phe Phe Arg			1248
20	240	245	250	
21				
22				
23	GCC AGT CCG AGT CCC ATC CGC ACC CCT CGG GCA GTG AGG CCA CTG AGG Ala Ser Pro Ser Pro Ile Arg Thr Pro Arg Ala Val Arg Pro Leu Arg			1296
24	255	260	265	
25				
26				
27	AGG AGG CAG CCG AAG AAA AGC AAC GAG CTG CCG CAG GCC AAC CGA CTC Arg Arg Gln Pro Lys Lys Ser Asn Glu Leu Pro Gln Ala Asn Arg Leu			1344
28	270	275	280	285
29				
30				
31	CCA GGG ATC TTT GAT GAC GTC CAC GGC TCC CAC GGC CGG CAG GTC TGC Pro Gly Ile Phe Asp Asp Val His Gly Ser His Gly Arg Gln Val Cys			1392
32	290	295	300	
33				
34				
35	CGT CGG CAC GAG CTC TAC GTC AGC TTC CAG GAC CTC GGC TGG CTG GAC Arg Arg His Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp Leu Asp			1440
36	305	310	315	
37				
38				
39	TGG GTC ATC GCT CCC CAA GGC TAC TCG GCC TAT TAC TGT GAG GGG GAG Trp Val Ile Ala Pro Gln Gly Tyr Ser Ala Tyr Tyr Cys Glu Gly Glu			1488
40	320	325	330	
41				
42				
43	TGC TCC TTC CCA CTG GAC TCC TGC ATG AAT GCC ACC AAC CAC GCC ATC Cys Ser Phe Pro Leu Asp Ser Cys Met Asn Ala Thr Asn His Ala Ile			1536
44	335	340	345	
45				
46				
47	CTG CAG TCC CTG GTG CAC CTG ATG AAG CCA AAC GCA GTC CCC AAG GCG Leu Gln Ser Leu Val His Leu Met Lys Pro Asn Ala Val Pro Lys Ala			1584
48	350	355	360	365
49				
50				
51	TGC TGT GCA CCC ACC AAG CTG AGC GCC ACC TCT GTG CTC TAC TAT GAC Cys Cys Ala Pro Thr Lys Leu Ser Ala Thr Ser Val Leu Tyr Tyr Asp			1632
52	370	375	380	
53				
54				
55	AGC AGC AAC AAC GTC ATC CTG CGC AAA GCC CGC AAC ATG GTG GTC AAG Ser Ser Asn Asn Val Ile Leu Arg Lys Ala Arg Asn Met Val Val Lys			1680
56	385	390	395	
57				
58				

1   GCC TGC GGC TGC CAC T GAGTCAGCCC GCCCAGCCCT ACTGCAG  
2   Ala Cys Gly Cys His  
3   400

1723

/CONNIE WONG/

Dated: October 20, 2006

---

James F. Haley, Jr. (Reg. No. 27,794)  
Karen Mangasarian (Reg. No. 43,772)  
Connie Wong (Reg. No. L0104)

Fish & Neave IP Group  
Ropes & Gray LLP  
1251 Avenue of the Americas  
New York, NY 10020-1104  
Tel.: (212) 596-9034  
Fax.: (212) 596-9090